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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/005,646

DATE: 04/16/2002

TIME: 14:13:38

Input Set : A:\Berlx87.app

Output Set: N:\CRF3\04162002\J005646.raw

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3 <110> APPLICANT: BRINGMANN, PETER W.
4   FAULDS, DARYL
5   MITROVIC, BRANISLAVA
6   SRINIVASAN, SUBHA
8 <120> TITLE OF INVENTION: NOVEL FIBROBLAST GROWTH FACTORS
10 <130> FILE REFERENCE: BERLX 87
12 <140> CURRENT APPLICATION NUMBER: 10/005,646
13 <141> CURRENT FILING DATE: 2001-12-07
15 <150> PRIOR APPLICATION NUMBER: 60/251,837
16 <151> PRIOR FILING DATE: 2000-12-08
18 <160> NUMBER OF SEQ ID NOS: 16
20 <170> SOFTWARE: PatentIn Ver. 2.1
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24 <212> TYPE: DNA
25 <213> ORGANISM: Unknown Organism
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29 <222> LOCATION: (1)..(633)
31 <220> FEATURE:
32 <223> OTHER INFORMATION: Description of Unknown Organism: FGF-21 nucleotide
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38   1           5           10           15
40 ttg ggc cag cag gtg ggt tcg cat ttc ctg ttg cct cct gcc ggg gag   96
41 Leu Gly Gln Gln Val Gly Ser His Phe Leu Leu Pro Pro Ala Gly Glu
42   20           25           30
44 cgg ccg ccg ctg ctg ggc gag cgc agg agc gcg gcg gag cgg agc gcg   144
45 Arg Pro Pro Leu Leu Gly Glu Arg Arg Ser Ala Ala Glu Arg Ser Ala
46   35           40           45
48 cgc ggc ggg ccg ggg gct gcg cag ctg gcg cac ctg cac ggc atc ctg   192
49 Arg Gly Gly Pro Gly Ala Ala Gln Leu Ala His Leu His Gly Ile Leu
50   50           55           60
52 cgc cgc ccg cag ctg tat tgc cgc acc ggc ttc cac ctg cag atc ctg   240
53 Arg Arg Arg Gln Leu Tyr Cys Arg Thr Gly Phe His Leu Gln Ile Leu
54   65           70           75           80
56 ccc gac ggc agc gtg cag ggc acc ccg cag gac cac agc ctg ttc ggt   288
57 Pro Asp Gly Ser Val Gln Gly Thr Arg Gln Asp His Ser Leu Phe Gly
58   85           90           95
60 atc ttg gaa ttc atc agt gtg gca gtg gga ctg gtc agt att aga ggt   336
61 Ile Leu Glu Phe Ile Ser Val Ala Val Gly Leu Val Ser Ile Arg Gly

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64 gtg gac agt ggt ctc tat ctt gga atg aat gac aaa gga gaa ctc tat 384
65 Val Asp Ser Gly Leu Tyr Leu Gly Met Asn Asp Lys Gly Glu Leu Tyr
66          115          120          125
68 gga tca gag aaa ctt act tcc gaa tgc atc ttt agg gag cag ttt gaa 432
69 Gly Ser Glu Lys Leu Thr Ser Glu Cys Ile Phe Arg Glu Gln Phe Glu
70          130          135          140
72 gag aac tgg tat aac acc tat tca tct aac ata tat aaa cat gga gac 480
73 Glu Asn Trp Tyr Asn Thr Tyr Ser Ser Asn Ile Tyr Lys His Gly Asp
74 145          150          155          160
76 act ggc cgc agg tat ttt gtg gca ctt aac aaa gac gga act cca aga 528
77 Thr Gly Arg Arg Tyr Phe Val Ala Leu Asn Lys Asp Gly Thr Pro Arg
78          165          170          175
80 gat ggc gcc agg tcc aag agg cat cag aaa ttt aca cat ttc tta cct 576
81 Asp Gly Ala Arg Ser Lys Arg His Gln Lys Phe Thr His Phe Leu Pro
82          180          185          190
84 aga cca gtg gat cca gaa aga gtt cca gaa ttg tac aag gac cta ctg 624
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89 Met Tyr Thr
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106 Leu Gly Gln Gln Val Gly Ser His Phe Leu Leu Pro Pro Ala Gly Glu
107 20 25 30
109 Arg Pro Pro Leu Leu Gly Glu Arg Arg Ser Ala Ala Glu Arg Ser Ala
110 35 40 45
112 Arg Gly Gly Pro Gly Ala Ala Gln Leu Ala His Leu His Gly Ile Leu
113 50 55 60
115 Arg Arg Arg Gln Leu Tyr Cys Arg Thr Gly Phe His Leu Gln Ile Leu
116 65 70 75 80
118 Pro Asp Gly Ser Val Gln Gly Thr Arg Gln Asp His Ser Leu Phe Gly
119 85 90 95
121 Ile Leu Glu Phe Ile Ser Val Ala Val Gly Leu Val Ser Ile Arg Gly
122 100 105 110
124 Val Asp Ser Gly Leu Tyr Leu Gly Met Asn Asp Lys Gly Glu Leu Tyr
125 115 120 125
127 Gly Ser Glu Lys Leu Thr Ser Glu Cys Ile Phe Arg Glu Gln Phe Glu
128 130 135 140
130 Glu Asn Trp Tyr Asn Thr Tyr Ser Ser Asn Ile Tyr Lys His Gly Asp

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131 145          150          155          160
133 Thr Gly Arg Arg Tyr Phe Val Ala Leu Asn Lys Asp Gly Thr Pro Arg
134          165          170          175
136 Asp Gly Ala Arg Ser Lys Arg His Gln Lys Phe Thr His Phe Leu Pro
137          180          185          190
139 Arg Pro Val Asp Pro Glu Arg Val Pro Glu Leu Tyr Lys Asp Leu Leu
140          195          200          205
142 Met Tyr Thr
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154 <222> LOCATION: (1)..(510)
156 <220> FEATURE:
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162 Met Arg Arg Arg Leu Trp Leu Gly Leu Ala Trp Leu Leu Leu Ala Arg
163 1 5 10 15
165 gcg ccg gac gcc gcg gga acc ccg agc gcg tcg cgg gga ccg cgc agc 96
166 Ala Pro Asp Ala Ala Gly Thr Pro Ser Ala Ser Arg Gly Pro Arg Ser
167 20 25 30
169 tac ccg cac ctg gag ggc gac gtg cgc tgg cgg cgc ctc ttc tcc tcc 144
170 Tyr Pro His Leu Glu Gly Asp Val Arg Trp Arg Arg Leu Phe Ser Ser
171 35 40 45
173 act cac ttc ttc ctg cgc gtg gat ccc ggc ggc cgc gtg cag ggc acc 192
174 Thr His Phe Phe Leu Arg Val Asp Pro Gly Gly Arg Val Gln Gly Thr
175 50 55 60
177 cgc tgg cgc cac ggc cag gac agc atc ctg gag atc cgc tct gta cac 240
178 Arg Trp Arg His Gly Gln Asp Ser Ile Leu Glu Ile Arg Ser Val His
179 65 70 75 80
181 gtg ggc gtc gtg gtc atc aaa gca gtg tcc tca ggc ttc tac gtg gcc 288
182 Val Gly Val Val Val Ile Lys Ala Val Ser Ser Gly Phe Tyr Val Ala
183 85 90 95
185 atg aac cgc cgg ggc cgc ctc tac ggg tcg cga ctc tac acc gtg gac 336
186 Met Asn Arg Arg Gly Arg Leu Tyr Gly Ser Arg Leu Tyr Thr Val Asp
187 100 105 110
189 tgc agg ttc cgg gag cgc atc gaa gag aac ggc cac aac acc tac gcc 384
190 Cys Arg Phe Arg Glu Arg Ile Glu Glu Asn Gly His Asn Thr Tyr Ala
191 115 120 125
193 tca cag cgc tgg cgc cgc cgc ggc cag ccc atg ttc ctg gcg ctg gac 432
194 Ser Gln Arg Trp Arg Arg Arg Gly Gln Pro Met Phe Leu Ala Leu Asp
195 130 135 140
197 agg agg ggg ggg ccc cgg cca ggc ggc cgg acg cgg cgg tac cac ctg 480
198 Arg Arg Gly Gly Pro Arg Pro Gly Gly Arg Thr Arg Arg Tyr His Leu

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199 145          150          155          160          513
201 tcc gcc cac ttc ctg ccc gtc ctg gtc tcc tga
202 Ser Ala His Phe Leu Pro Val Leu Val Ser
203          165          170
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212 <223> OTHER INFORMATION: Description of Unknown Organism: FGF-23 amino acid
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219 Ala Pro Asp Ala Ala Gly Thr Pro Ser Ala Ser Arg Gly Pro Arg Ser
220          20          25          30
222 Tyr Pro His Leu Glu Gly Asp Val Arg Trp Arg Arg Leu Phe Ser Ser
223          35          40          45
225 Thr His Phe Phe Leu Arg Val Asp Pro Gly Gly Arg Val Gln Gly Thr
226          50          55          60
228 Arg Trp Arg His Gly Gln Asp Ser Ile Leu Glu Ile Arg Ser Val His
229  65          70          75          80
231 Val Gly Val Val Val Ile Lys Ala Val Ser Ser Gly Phe Tyr Val Ala
232          85          90          95
234 Met Asn Arg Arg Gly Arg Leu Tyr Gly Ser Arg Leu Tyr Thr Val Asp
235          100         105         110
237 Cys Arg Phe Arg Glu Arg Ile Glu Glu Asn Gly His Asn Thr Tyr Ala
238          115         120         125
240 Ser Gln Arg Trp Arg Arg Arg Gly Gln Pro Met Phe Leu Ala Leu Asp
241          130         135         140
243 Arg Arg Gly Gly Pro Arg Pro Gly Gly Arg Thr Arg Arg Tyr His Leu
244 145          150          155          160
246 Ser Ala His Phe Leu Pro Val Leu Val Ser
247          165          170
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253 <212> TYPE: PRT
254 <213> ORGANISM: Unknown Organism
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265          20          25          30
267 Leu Ser Asp His Leu Gly Gln Ser Glu Ala Gly Gly Leu Pro Arg Gly
268          35          40          45
270 Pro Ala Val Thr Asp Leu Asp His Leu Lys Gly Ile Leu Arg Arg Arg

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271      50      55      60
273 Gln Leu Tyr Cys Arg Thr Gly Phe His Leu Glu Ile Phe Pro Asn Gly
274 65      70      75      80
276 Thr Ile Gln Gly Thr Arg Lys Asp His Ser Arg Phe Gly Ile Leu Glu
277      85      90      95
279 Phe Ile Ser Ile Ala Val Gly Leu Val Ser Ile Arg Gly Val Asp Ser
280      100      105      110
282 Gly Leu Tyr Leu Gly Met Asn Glu Lys Gly Glu Leu Tyr Gly Ser Glu
283      115      120      125
285 Lys Leu Thr Gln Glu Cys Val Phe Arg Glu Gln Phe Glu Glu Asn Trp
286      130      135      140
288 Tyr Asn Thr Tyr Ser Ser Asn Leu Tyr Lys His Val Asp Thr Gly Arg
289 145      150      155      160
291 Arg Tyr Tyr Val Ala Leu Asn Lys Asp Gly Thr Pro Arg Glu Gly Thr
292      165      170      175
294 Arg Thr Lys Arg His Gln Lys Phe Thr His Phe Leu Pro Arg Pro Val
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315      20      25      30
317 Phe Leu Asn Glu Arg Leu Gly Gln Ile Glu Gly Lys Leu Gln Arg Gly
318      35      40      45
320 Ser Pro Thr Asp Phe Ala His Leu Lys Gly Ile Leu Arg Arg Arg Gln
321      50      55      60
323 Leu Tyr Cys Arg Thr Gly Phe His Leu Glu Ile Phe Pro Asn Gly Thr
324 65      70      75      80
326 Val His Gly Thr Arg His Asp His Ser Arg Phe Gly Ile Leu Glu Phe
327      85      90      95
329 Ile Ser Leu Ala Val Gly Leu Ile Ser Ile Arg Gly Val Asp Ser Gly
330      100      105      110
332 Leu Tyr Leu Gly Met Asn Glu Arg Gly Glu Leu Tyr Gly Ser Lys Lys
333      115      120      125
335 Leu Thr Arg Glu Cys Val Phe Arg Glu Gln Phe Glu Glu Asn Trp Tyr
336      130      135      140
338 Asn Thr Tyr Ala Ser Thr Leu Tyr Lys His Ser Asp Ser Glu Arg Gln
339 145      150      155      160
341 Tyr Tyr Val Ala Leu Asn Lys Asp Gly Ser Pro Arg Glu Gly Tyr Arg
342      165      170      175

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VERIFICATION SUMMARY

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DATE: 04/16/2002

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Input Set : A:\Berlx87.app

Output Set: N:\CRF3\04162002\J005646.raw

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L:495 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:13